

PURA18WO.ST25  
SEQUENCE LISTING

<110> PURATOS N.V.  
<120> MYROTHECIUM SP. TRANSFORMATION AND EXPRESSION SYSTEM  
<130> P.PURA18.WO  
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<223> ITS1 primer

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<400> 5  
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19

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<213> Myrothecium

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gaacgggacg ccatagaggg tgagagcccc gtctggtcgg acaccgagcc tctgtaaagc 180  
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cgttgcgtaa taccctgcgg tggactgagg tccgcgcttc tgcaaggatg ctggcgtaat 540  
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gggtgtaaaa cccctacgcg taatgaaagt gaacgcaggt gagagcttcg gcgcatcatc 660  
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<212> DNA  
<213> Myrothecium

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<220>  
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<223> 28s rDNA sequence of the strain MUCL11831

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gacgggacgc cggagagggg gagagccccg tcaggttgga caccaagcct atgtaaatct 180  
ccttcgacga gtcgagtagt ttgggaatgc tgctctaaat gggaggtata tgtcttctaa 240  
agctaaatac cggccagaga ccgatagcgc acaagtagag tgatcgaaag atgaaaagca 300  
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<210> 9  
<211> 1012  
<212> DNA  
<213> Myrothecium

<220>  
<221> misc\_feature  
<223> 28s rDNA sequence of the strain CBS449.71

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aacgggacgc catagagggg gagagccccg tctggctgga caccgagcct ctgtaaagct 180  
ccttcgacga gtcgagtagt ttgggaatgc tgctcaaat gggaggtata tgtcttctaa 240  
agctaaatac cggccagaga ccgatagcgc acaagtagag tgatcgaaag atgaaaagca 300  
ctttgaaaag agagttaaact agcacgtgaa attgttgaaa gggaagcggt tatgaccaga 360  
cttggcccgg ttgatcatcc agccttctgg ctggtgcact ctgccggtcc aggccagcat 420

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cagttcgtcg cgggggataa aggtttcggg aatgtagctc ctccgggagt gttatagccc 480
gttgcgtaat accctgcggt ggactgaggt ccgcgctctg caaggatgct ggcgtaatgg 540
tcatcaacga cccgtcttga aacacggacc aaggagtcgt cttcgtatgc gagtgttcgg 600
gtgtaaaacc cctacgcgta atgaaagtga acgcaggtga gagcttcggc gcatcatcga 660
ccgatcctga tgttctcggg tggatttgag taagagcata cggggccgga cccgaaagaa 720
ggtgaactat gcctgtatag ggtgaagcca gaggaaactc tgggtggaggc tcgcagcggg 780
tctgacgtgc aaatcgatcg tcaaatatgg gcatgggggc gaaagactaa tcgaaccttc 840
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ggtaaagcga atgattaggg actcgggggc gctatttagc cttcatccat tctcaaactt 960
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<210> 10  
 <211> 1038  
 <212> DNA  
 <213> Myrothecium

<220>  
 <221> misc\_feature  
 <223> 28s rDNA sequence of the strain IMI140595

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aacgggacgc catagagggt gagagccccg tctggtcgga caccgagcct ctgtaaaagt 180
ccttcgacga gtcgagtagt ttgggaatgc tgctcaaaat gggaggtata tgtcttctaa 240
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cagttcgcg cgggggataa aggtttcggg aatgtggctc ctccgggagt gttatagccc 480
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tagtgggcca tttttggt 1038

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<210> 11  
 <211> 1044  
 <212> DNA  
 <213> Myrothecium

<220>  
 <221> misc\_feature  
 <223> 28S rDNA sequence of the strain IMI29040

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 gaacgggacg ccatagaggg tgagagcccc gtctggctcg acaccgagcc tctgtaaagc 180  
 tccttcgacg agtcgagtag tttgggaatg ctgctcaaaa tgggaggtat atgtcttcta 240  
 aagctaaata cgggccagag accgatagcg cacaagtaga gtgatcgaaa gatgaaaagc 300  
 actttgaaaa gagagttaaa tagcacgtga aattgttgaa agggaagcgt ttatgaccag 360  
 acttggcccg gttgatcatc cagcgttctc gctggtgcac tctgccggtc caggccagca 420  
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 cccgttgtgt aataccctgc ggtggactga ggtccgcgct ctgcaaggat gctggcgtaa 540  
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 tagtgggcca tttttggtaa gcag 1044

<210> 12  
 <211> 445  
 <212> DNA  
 <213> Myrothecium

<220>  
 <221> misc\_feature  
 <223> ITS sequence of the strain MUCL39210

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 aacggatctc ttggttctgg catcgatgaa gaacgcagcg aaatgcgata agtaatgtga 180  
 attgcagaat tcagtgaatc atcgaatctt tgaacgcaca ttgcgccccg cagtattctg 240

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gcgggcatgc ctgttcgagc gtcatttcaa ccctcaggcc ccagtgctt ggcgttggg 300  
 atcggcacca gggcgccgc gcaagcggc tccccgccg cccgaaatc tagtgccgg 360  
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 ctgccgttaa acacccact tctga 445

<210> 13  
 <211> 459  
 <212> DNA  
 <213> Myrothecium

<220>  
 <221> misc\_feature  
 <223> ITS sequence of the strain MUCL11831

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 ttaacaacgg atctcttggc tctggcatcg atgaagaacg cagcgaaatg cgataagtaa 180  
 tgtgaattgc agaattcagt gaatcatcga atctttgaac gcacattgcg ccgcgagta 240  
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 cgcggcgctg gtgttgggga tcggccctaa accgccgtcc ccaaattca gtggcggtct 360  
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 <212> DNA  
 <213> Myrothecium

<220>  
 <221> misc\_feature  
 <223> ITS sequence of the strain CBS449.71

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 ttatgtcttt agtggttttc tcctctgagt gacacataaa caaataaata aaaactttca 120  
 acaacggatc tcttggttct ggcatcgatg aagaacgcag cgaaatgcga taagtaatgt 180  
 gaattgcaga attcagtga tcatcgaatc tttgaacgca cattgcgccc gccagtattc 240  
 tggcgggcat gcctgttcga gcgtcatttc aaccctcagg ccccagtgct ctggtgttgg 300  
 ggatcgcccc agccttctcg caaggccgcc ggccccgaaa tctagtggcg gtctcgctgt 360  
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 aaa 423

<210> 15  
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<212> DNA  
<213> Myrothecium

<220>  
<221> misc\_feature  
<223> ITS sequence of the strain IMI140595

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aacggatctc ttggttctgg catcgatgaa gaacgcagcg aaatgcgata agtaatgtga 180  
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atcggtcag gggcgaccgc gcaagcggcc gcttcccgcc ggccccgaaa tctagtggcg 360  
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ccctgccgta aaacacccca cttct 445

<210> 16  
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<212> DNA  
<213> Myrothecium

<220>  
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<223> ITS sequence of the strain IMI290405

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gaattgcaga attcagtga tcatcgaatc ttgaaacgca cattgcgccc gccagtattc 240  
tggcgggcat gcctgttcga gcgtcatttc aacctcagg ccccagtcg ctggcggttg 300  
ggatcggcag cagggcgtca agcccgccg ccccgaaatc tagtggcgg ctcgctgtag 360  
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acacccact tctg 434

<210> 17  
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<212> DNA  
<213> Artificial

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<223> AMY1 primer

<400> 17  
ggaattccac agaaggcatt tatg 24

<210> 18  
<211> 23

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<212> DNA  
<213> Artificial  
  
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<223> AMY2 primer  
  
<400> 18  
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23

<210> 19  
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<220>  
<223> Gpd1 primer

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<223> n is A, C, T or G

<220>  
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<223> n is dInosine

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<220>  
<223> Gpd2 primer

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20

<210> 21  
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<220>  
<223> Gpd3 primer

<220>  
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<223> n is A, C, T or G

<220>  
<221> misc\_feature  
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23



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<220>  
 <223> Gpd4 primer

<220>  
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23

<210> 23  
 <211> 836  
 <212> DNA  
 <213> Myrothecium

<220>  
 <221> misc\_feature  
 <223> gpd gene sequence of the strain MUCL11831

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 atgatggtgt acttgctcgtt gaggaccttg gcgaggggag ccaggcagtt ggtggtgcac 180  
 gaggcgttgg agatgacatc ggcgctgccg tcgtaggctt tctcgttgac gcccatcacg 240  
 tacatggggg catcggcgga gggggcggag atgatgacct tcttggcacc gccagcaagg 300  
 tgagccttgg ccttgctcgtt ggtggtgaag acaccggtgg actcgacaat gtactcggcg 360  
 ccggtctcct tccaggggat ggaggcggg tcacgctcgg tgtagaagcg gaccttcttg 420  
 ccgttgacgc tcaggtcagc gccatcggcc tcgacctcac ccttgaagag accgtgggtg 480  
 gagtcatact tgagcatgta ggcctagatg gtggtcagct aaagcgctca tttcaagaca 540  
 aagaaagcag atgtcaaggt tggcgggaaa agacgatgga ggggcacggg tttggacatg 600  
 gttgcaggta ggtggggtgc aacggcccat gtcattgcaa gcatgccatg tcgggttttg 660  
 cccctcggat tggatttctt ttttcgcgcc gcatcatgta aagtgggggg aggggcagca 720  
 ctcacggcgt acttggtctc gatgaagggg tcgttgacgg cgacaatctc aatgtcgggg 780  
 tgctcgacgg cgttgcggaa gacgatacga ccgatgcggc cgaaccatt gatccc 836

<210> 24  
 <211> 954  
 <212> DNA  
 <213> Myrothecium

<220>  
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 <223> gpd gene sequence of the strain CBS449.71

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 tgatggtgaa cttgtcgttg atgaccttg cgaggggagc caggcagttg gtggtgcaag 180  
 aagcgttga gatgacgtc gcgctgccgt cgtaggtctc ctcgttgaca cccataacgt 240  
 acatgggggc atcggcggag ggagcagaga tgatgacctt cttggcacca cccttcaagt 300  
 gagcagcagc cttgtccttg gtggtgaaga caccagtga ctcgacgat tactcggcgc 360  
 cagtctcctt ccaggggatg gcagcggggt cgcgctcagt gtagaagcgg accttcttgc 420  
 cgttgacagt gaggtcggca ccatcgacgg agacctcacc cttgaagaga ccgtgggtag 480  
 agtcatactt gagcatgtag gcctagtga caggggtggt tagcggaatg gccggcagag 540  
 agagagtaat tgcggcatga cgaggcgttg gagggaggag cagtcctctg ccatgacgat 600  
 agcattggct attgattcat tcgccgcctt gacagagggc tcgttgaact gcaccaacgc 660  
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 gcaagtgcatt ggtggactgc agctcgcttg cctagttgtt ggctgaaggg aaacagcact 840  
 tacagcgtac ttgggtctaa tgaagggatc gttgacggca acgatctcga cgtcgtcgtg 900  
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 atgatggtga acttgtcgtg aatgaccttg gcgagaggag ccaggcagtt ggtggtgcag 180  
 gaggcgttgg agatgacgtc ggcgctgccg tcgtaggtct cctcgttgac acccataacg 240  
 tacatgggag catcagcaga gggggcagag atgatgacct tcttggcacc acccttcaag 300  
 tgagcagcgg cttgtcctt ggtggtgaag acaccggttg actcgacgat gtagtcggcg 360  
 ccagtctcct tccaagggat ggcagcgggg tcacgctcag ttagaagcg gaccttcttg 420  
 ccgttgacgg tcaggctcag gccatcgacg gtgacctcac cttgaagac gccgtgggtg 480  
 gagtcatact tgagcatgta ggcctatgcg tggatggttg tgggaagcat gagtgaattg 540  
 gagggattgc gtgagggtga tgaagcatca ttgtggtgtg tcaatggggc tgtttctgct 600  
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 agacggcggc gcatgatatc atggaggggc aaatattgac gcgctgatga tagtggggtg 720

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atttttggag gcacctggtt ttgtctttgg ttgcattttt tctgcccctc actcggtcgg 780  
 tccgtgtctg cggcgcgct ctgcccctcc tctgtctgca cagagtgcac gctgggctgc 840  
 agccagctcc gttgcccgt cgctcgctcg cctgcgtgcc ttgtcccttt ggagctgagg 900  
 ggaaagaggt gggatcgaga tcacaatcaa aaggttgtag tcacagcgta ggtgggctca 960  
 atgaagggat cgttgacggc aacgatctcg acgtcggagt gctcgacggc gttgcggaag 1020  
 acgatacgac caatgcggcc gaaccattg atacc 1055

<210> 26  
 <211> 850  
 <212> DNA  
 <213> Myrothecium

<220>  
 <221> misc\_feature  
 <223> gpd gene sequence of Myrothecium gramineum (Xepiculopsis graminea)  
 MUCL39210

<400> 26  
 gccgtcgagc actccgacgt cgagatcggt gccgtcaacg accccttcac tgagcccaag 60  
 tacgtgtaa gtgtgcttc tgcttcccct cagtcgacga gcgagcccaa agccgagctg 120  
 cagctagcgg agccatgcgc tgcttgcacg cactgcata acagcagcta gaggaggggt 180  
 acacggccgc gcgcgcagac acacatacaa caccaccacc accaaaagga ggggcagaaa 240  
 aaatccagca ttgtccgatt tcacccacc atctcacgtc aaccaatttg cccctccatg 300  
 atatcatgtg tccgcgcca gctcaacacg tccacctcct ctggccaatg gcgagcgcat 360  
 tgatgctttg atgagcggaa acgacgctga ggccctcagc ctcgtcgtcg ctgccgctgc 420  
 cgccgcgcgc cgctcacgca tcggcgggct cccgtcgtcg ggcttcaatt gacatgacat 480  
 gatgcatggc caccgtgcta accaccctg tgtctgtccg ataggcctac atgctcaagt 540  
 atgactctac ccacggtctc ttcaaggggt aggtcaccgt cgatggcgat gacctgaccg 600  
 tcaacggcaa gaaggtccgc ttctacactg agcgtgacct cgccgccatc ccctggaagg 660  
 agactgggtg cgagtacatt gtcgagtcca ccggtgtctt caccaccaag gacaaggctg 720  
 ctgctcacct gaaggggtgt gccagaagg tcatcatctc tgccccctct gccgatgcc 780  
 ccatgtacgt tatgggtgtc aacgaggaga cctacgacgg cagcgccgac gtcattctca 840  
 acgcttcttg 850

<210> 27  
 <211> 130  
 <212> PRT  
 <213> Myrothecium

<220>  
 <221> MISC\_FEATURE  
 <223> glyceraldehyde 3-P dehydrogenase sequence of Myrothecium  
 gramineum (Xepiculopsis graminea) MUCL39210

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&lt;400&gt; 27

Ala Val Glu His Ser Asp Val Glu Ile Val Ala Val Asn Asp Pro Phe  
 1 5 10 15

Ile Glu Pro Lys Tyr Ala Ala Tyr Met Leu Lys Tyr Asp Ser Thr His  
 20 25 30

Gly Leu Phe Lys Gly Glu Val Thr Val Asp Gly Asp Asp Leu Thr Val  
 35 40 45

Asn Gly Lys Lys Val Arg Phe Tyr Thr Glu Arg Asp Pro Ala Ala Ile  
 50 55 60

Pro Trp Lys Glu Thr Gly Ala Glu Tyr Ile Val Glu Ser Thr Gly Val  
 65 70 75 80

Phe Thr Thr Lys Asp Lys Ala Ala Ala His Leu Lys Gly Gly Ala Lys  
 85 90 95

Lys Val Ile Ile Ser Ala Pro Ser Ala Asp Ala Pro Met Tyr Val Met  
 100 105 110

Gly Val Asn Glu Glu Thr Tyr Asp Gly Ser Ala Asp Val Ile Ser Asn  
 115 120 125

Ala Ser  
 130

<210> 28  
 <211> 21  
 <212> DNA  
 <213> Artificial

<220>  
 <223> hphpCSN431 primer

<400> 28  
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21

<210> 29  
 <211> 18  
 <212> DNA  
 <213> Artificial

<220>  
 <223> hphpCSN432 primer

<400> 29  
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18

<210> 30  
 <211> 16  
 <212> DNA  
 <213> Artificial

&lt;220&gt;

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<223> GPD2 primer  
 <400> 30  
 tctggcatgc ggagag 16

<210> 31  
 <211> 16  
 <212> DNA  
 <213> Artificial

<220>  
 <223> AMY5 primer  
 <400> 31  
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<210> 32  
 <211> 850  
 <212> DNA  
 <213> Myrothecium

<220>  
 <221> CDS  
 <222> (1)..(66)

<220>  
 <221> misc\_feature  
 <222> (1)..(850)  
 <223> partial nucleotide sequence and its deduced protein sequence of  
 the Myrothecium gramineum MUCL39210 glyceraldehyde-3-P  
 dehydrogenase gene

<220>  
 <221> CDS  
 <222> (525)..(848)

<400> 32  
 gcc gtc gag cac tcc gac gtc gag atc gtt gcc gtc aac gac ccc ttc 48  
 Ala Val Glu His Ser Asp Val Glu Ile Val Ala Val Asn Asp Pro Phe  
 1 5 10 15

att gag ccc aag tac gct gtaagtgctg cttctgcttc ccctcagtcg 96  
 Ile Glu Pro Lys Tyr Ala  
 20

acgagcgagc ccaaagccga gctgcagcta gcggagccat gcgctgcctg catgccactg 156  
 cataacagca gctagaggag ggggtacacgg ccgcgcgcgc agacacacat acaacaccac 216  
 caccaccaaaggaggggcga gaaaaaatcc agcattgtcc gatttcaccc caccatctca 276  
 cgtcaaccaa tttgcccctc catgatatca tgtgtccgcg cccagctcaa cacgtccacc 336  
 tcctctggcc aatggcgagc gcattgatgc tttgatgagc ggaaacgacg ctgaggccct 396  
 cagcctcgtc gtcgctgccg ctgccgccgc gcgccgtca cgcacggcg ggctcccgtc 456  
 gctgggcttc aattgacatg acatgatgca tggccaccgt gctaaccacc cctgtgtctg 516  
 tccgatag gcc tac atg ctc aag tat gac tct acc cac ggt ctc ttc aag 566  
 Ala Tyr Met Leu Lys Tyr Asp Ser Thr His Gly Leu Phe Lys  
 25 30 35

ggt gag gtc acc gtc gat ggc gat gac ctg acc gtc aac ggc aag aag 614  
 Gly Glu Val Thr Val Asp Gly Asp Asp Leu Thr Val Asn Gly Lys Lys

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40 45 50  
 gtc cgc ttc tac act gag cgt gac ccc gcc gcc atc ccc tgg aag gag 662  
 Val Arg Phe Tyr Thr Glu Arg Asp Pro Ala Ala Ile Pro Trp Lys Glu  
 55 60 65  
 act ggt gcc gag tac att gtc gag tcc acc ggt gtc ttc acc acc aag 710  
 Thr Gly Ala Glu Tyr Ile Val Glu Ser Thr Gly Val Phe Thr Thr Lys  
 70 75 80  
 gac aag gct gct gct cac ctg aag ggt ggt gcc aag aag gtc atc atc 758  
 Asp Lys Ala Ala Ala His Leu Lys Gly Gly Ala Lys Lys Val Ile Ile  
 85 90 95 100  
 tct gcc ccc tct gcc gat gcc ccc atg tac gtt atg ggt gtc aac gag 806  
 Ser Ala Pro Ser Ala Asp Ala Pro Met Tyr Val Met Gly Val Asn Glu  
 105 110 115  
 gag acc tac gac ggc agc gcc gac gtc atc tcc aac gct tct tg 850  
 Glu Thr Tyr Asp Gly Ser Ala Asp Val Ile Ser Asn Ala Ser  
 120 125 130

<210> 33  
 <211> 22  
 <212> PRT  
 <213> Myrothecium

<400> 33

Ala Val Glu His Ser Asp Val Glu Ile Val Ala Val Asn Asp Pro Phe  
1 5 10 15

Ile Glu Pro Lys Tyr Ala  
20

<210> 34  
 <211> 108  
 <212> PRT  
 <213> Myrothecium

<400> 34

Ala Tyr Met Leu Lys Tyr Asp Ser Thr His Gly Leu Phe Lys Gly Glu  
1 5 10 15

Val Thr Val Asp Gly Asp Asp Leu Thr Val Asn Gly Lys Lys Val Arg  
20 25 30

Phe Tyr Thr Glu Arg Asp Pro Ala Ala Ile Pro Trp Lys Glu Thr Gly  
35 40 45

Ala Glu Tyr Ile Val Glu Ser Thr Gly Val Phe Thr Thr Lys Asp Lys  
50 55 60

Ala Ala Ala His Leu Lys Gly Gly Ala Lys Lys Val Ile Ile Ser Ala  
65 70 75 80

Pro Ser Ala Asp Ala Pro Met Tyr Val Met Gly Val Asn Glu Glu Thr  
85 90 95

PURA18WO.ST25

Tyr Asp Gly Ser Ala Asp Val Ile Ser Asn Ala Ser  
 100 105

<210> 35  
 <211> 204  
 <212> PRT  
 <213> Myrothecium

<220>  
 <221> MISC\_FEATURE  
 <223> partial GPD protein sequence from the strain MUCL39210  
 <400> 35

Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Ile Val Phe Arg Asn Ala  
 1 5 10 15

Val Glu His Pro Asp Ile Glu Ile Val Ala Val Asn Asp Pro Phe Ile  
 20 25 30

Glu Thr Lys Tyr Ala Ala Tyr Met Leu Lys Tyr Asp Ser Thr His Gly  
 35 40 45

Leu Phe Lys Gly Glu Val Glu Ala Asp Gly Ala Asp Leu Ser Val Asn  
 50 55 60

Gly Lys Lys Val Arg Phe Tyr Thr Glu Arg Asp Pro Ala Ser Ile Pro  
 65 70 75 80

Trp Lys Glu Thr Gly Ala Glu Tyr Ile Val Glu Ser Thr Gly Val Phe  
 85 90 95

Thr Thr Thr Asp Lys Ala Lys Ala His Leu Ala Gly Gly Ala Lys Lys  
 100 105 110

Val Ile Ile Ser Ala Pro Ser Ala Asp Ala Pro Met Tyr Val Met Gly  
 115 120 125

Val Asn Glu Lys Thr Tyr Asp Gly Ser Ala Asp Val Ile Ser Asn Ala  
 130 135 140

Ser Cys Thr Thr Asn Cys Leu Ala Pro Leu Ala Lys Val Leu Asn Asp  
 145 150 155 160

Lys Tyr Thr Ile Ile Glu Gly Leu Met Thr Thr Val His Ser Tyr Thr  
 165 170 175

Ala Thr Gln Lys Thr Val Asp Gly Pro Ser Ala Lys Asp Trp Arg Gly  
 180 185 190

Gly Arg Gly Ala Ala Gln Asn Ile Ile Pro Thr Thr  
 195 200

PURA18WO.ST25

<210> 36  
 <211> 204  
 <212> PRT  
 <213> Myrothecium

<220>  
 <221> MISC\_FEATURE  
 <223> partial GPD protein sequence from the strain MUCL11831

<400> 36

Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Ile Val Phe Arg Asn Ala  
 1 5 10 15

Val Glu His Asp Asp Val Glu Ile Val Ala Val Asn Asp Pro Phe Ile  
 20 25 30

Glu Pro Lys Tyr Ala Ala Tyr Met Leu Lys Tyr Asp Ser Thr His Gly  
 35 40 45

Leu Phe Lys Gly Glu Val Ser Val Asp Gly Ala Asp Leu Thr Val Asn  
 50 55 60

Gly Lys Lys Val Arg Phe Tyr Thr Glu Arg Asp Pro Ala Ala Ile Pro  
 65 70 75 80

Trp Lys Glu Thr Gly Ala Glu Tyr Ile Val Glu Ser Thr Gly Val Phe  
 85 90 95

Thr Thr Lys Asp Lys Ala Ala Ala His Leu Lys Gly Gly Ala Lys Lys  
 100 105 110

Val Ile Ile Ser Ala Pro Ser Ala Asp Ala Pro Met Tyr Val Met Gly  
 115 120 125

Val Asn Glu Glu Thr Tyr Asp Gly Ser Ala Asp Val Ile Ser Asn Ala  
 130 135 140

Ser Cys Thr Thr Asn Cys Leu Ala Pro Leu Ala Lys Val Ile His Asp  
 145 150 155 160

Lys Phe Thr Ile Ile Glu Gly Leu Met Thr Thr Val His Ser Thr Leu  
 165 170 175

Pro Pro Arg Arg Pro Leu Thr Val Pro Pro Pro Arg Thr Gly Ala Val  
 180 185 190

Ala Val Val Leu Pro Arg Thr Ser Ser Pro Ala Ala  
 195 200

<210> 37  
 <211> 204  
 <212> PRT



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&lt;213&gt; Myrothecium

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;223&gt; partial GPD protein sequence from the strain CBS449.71

&lt;400&gt; 37

Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Ile Val Phe Arg Asn Ala  
1 5 10 15

Val Glu His Ser Asp Val Glu Ile Val Ala Val Asn Asp Pro Phe Ile  
20 25 30

Glu Pro Thr Tyr Ala Ala Tyr Met Leu Lys Tyr Asp Ser Thr His Gly  
35 40 45

Val Phe Lys Gly Glu Val Thr Val Asp Gly Ala Asp Leu Thr Val Asn  
50 55 60

Gly Lys Lys Val Arg Phe Tyr Thr Glu Arg Asp Pro Ala Ala Ile Pro  
65 70 75 80

Trp Lys Glu Thr Gly Ala Asp Tyr Ile Val Glu Ser Thr Gly Val Phe  
85 90 95

Thr Thr Lys Asp Lys Ala Ala Ala His Leu Lys Gly Gly Ala Lys Lys  
100 105 110

Val Ile Ile Ser Ala Pro Ser Ala Asp Ala Pro Met Tyr Val Met Gly  
115 120 125

Val Asn Glu Glu Thr Tyr Asp Gly Ser Ala Asp Val Ile Ser Asn Ala  
130 135 140

Ser Cys Thr Thr Asn Cys Leu Ala Pro Leu Ala Lys Val Ile His Asp  
145 150 155 160

Lys Phe Thr Ile Ile Glu Gly Leu Met Thr Thr Val His Ser Tyr Thr  
165 170 175

Ala Thr Gln Lys Thr Val Asp Gly Pro Ser Ala Lys Asp Trp Arg Gly  
180 185 190

Gly Arg Gly Ala Ala Gln Asn Ile Ile Pro Ser Thr  
195 200